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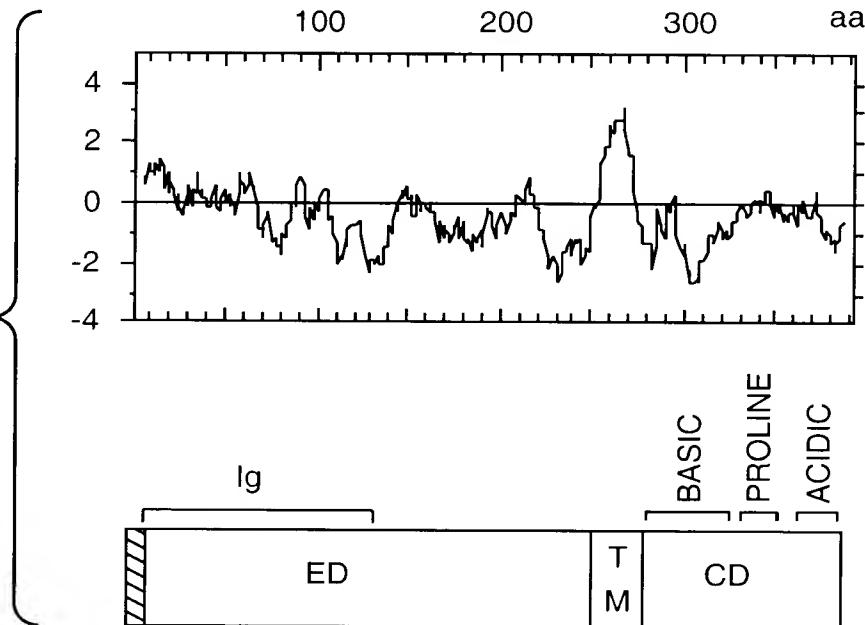
FIG. 1

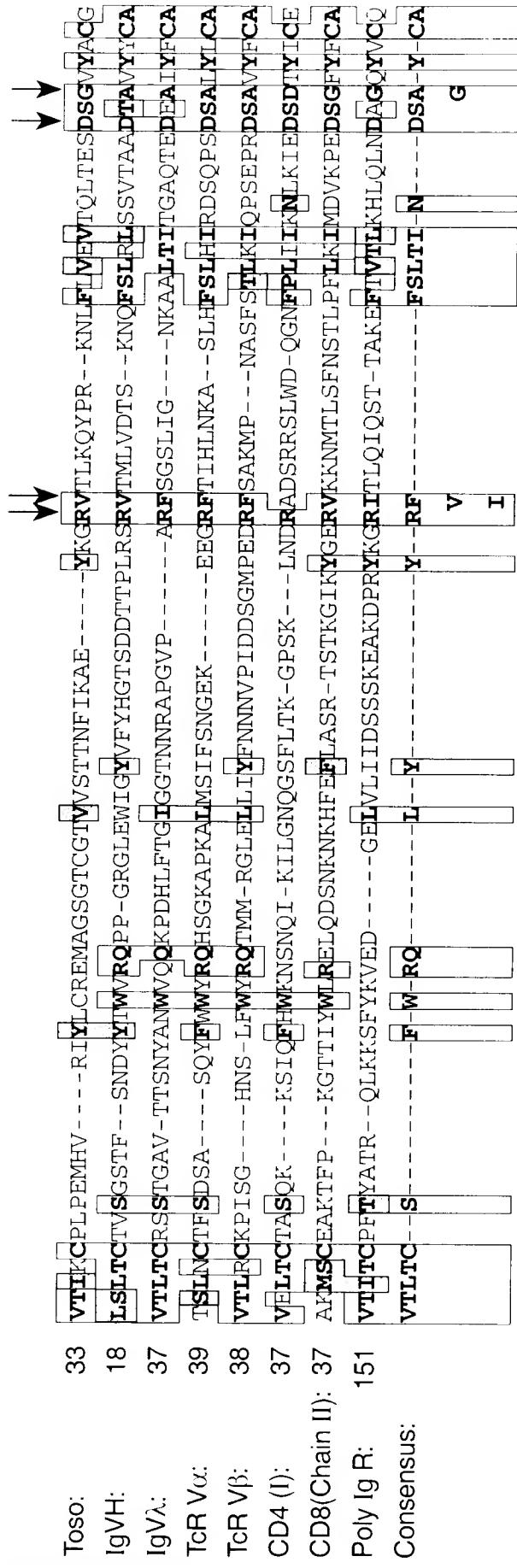
Coding region: Capitalized

Leader sequence: Underlined

Transmembrane region: Double underlined

1 **MDFWLWPLYF LPVSGALRIL PEVKVEGELG GSVTIK CPLP EMHVRIYLCR**
 51 **EMAGSGTCGT VVSTTNFIKA EYKGRVTLKQ YPRKNLFLVE VTQLTESD SG**
 101 **VYACGAGMNT DRGKTQKVTL NVHSEYEPSW EEQPMPETPK WFHLPYLFQM**
 151 **PAYASSSKFV TRVTTPAQRG KVPPVHHSSP TTQITHRPRV SRASSVAGDK**
 201 **PRTFLPSTTA SKISALEGLL KPQTPSYNHH TRLHRQRALD YGSQSGREGQ**
 251 **GFHILIPITL GLFLLALLGL VVKRAVERRK ALSRRARRLA VRMRALESSQ**
 301 **RPRGSPPRPRS QNNIYSACPR RARGADAAGT GEAPVPGPGA PLPPAPLQVS**
 351 **ESPWLHAPSL KTSCEYVSLY HQPAAMMEDS DSDDYINVPA**

FIG._2a**FIG._2b**



Toso: 300 FAST kinase: 2 Acid SMase: 1 Consensus:

QRFRGSPPRRSQNNTYSACPRRARGADAAAGTGEAFVPPGP	GAPI
FPRRGEPGPRA	-----PRPTEGATCA
MPPRYGASILRQSCPRSGREQQGDGTACAFGLIWMGLV	-----SPNSML

Toso: 351 Op-IAP: 162 IRS-1: 881 Acid SMase: 349

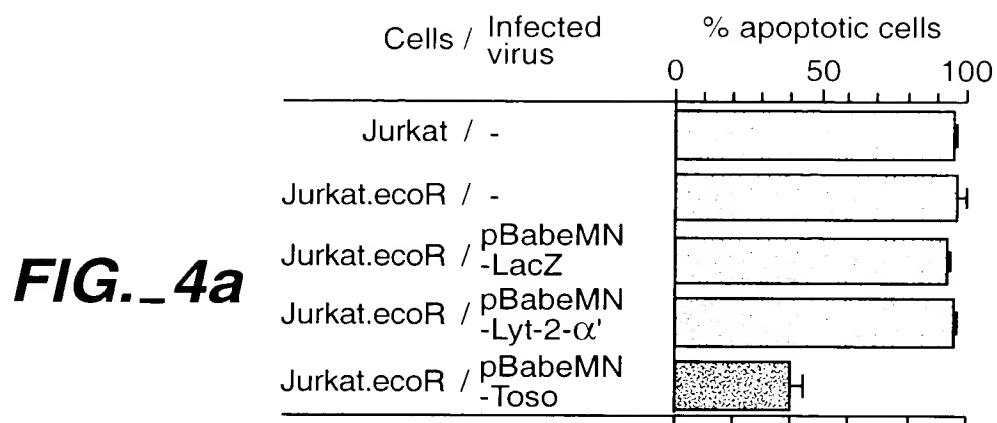
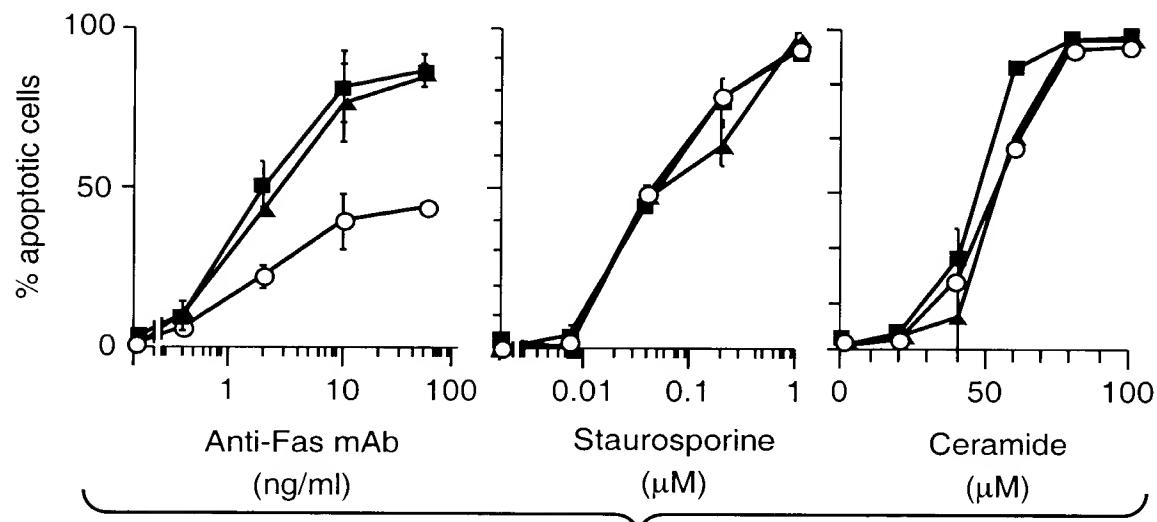
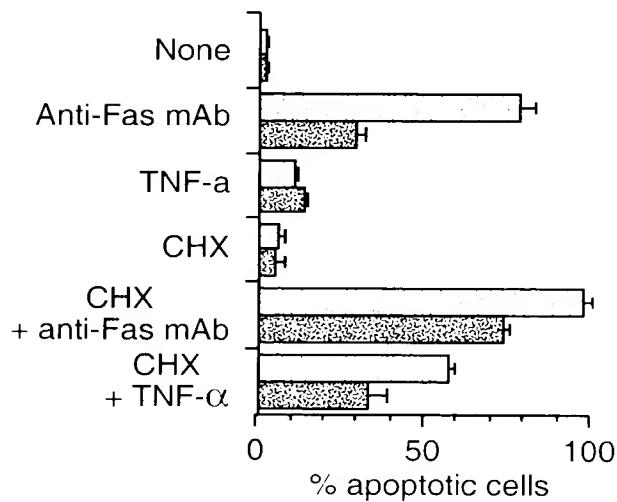
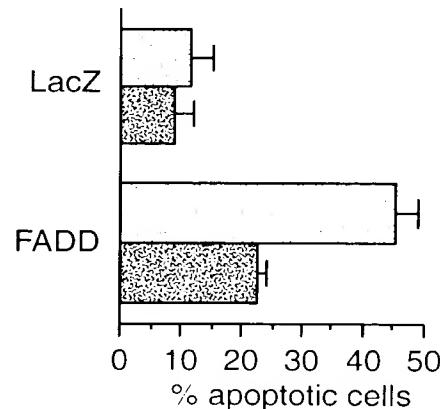
ESPWLHAPSILKTSCERYVSL	-----
DAPWQOQHARWYDRCEYVLL	-----
QQPLLHPPEEKS	PGEEYVNT
WEPWLPAEAALRT	-----LRIGGFY

Toso: 372 Op-IAP: 192 IRS-1: 928

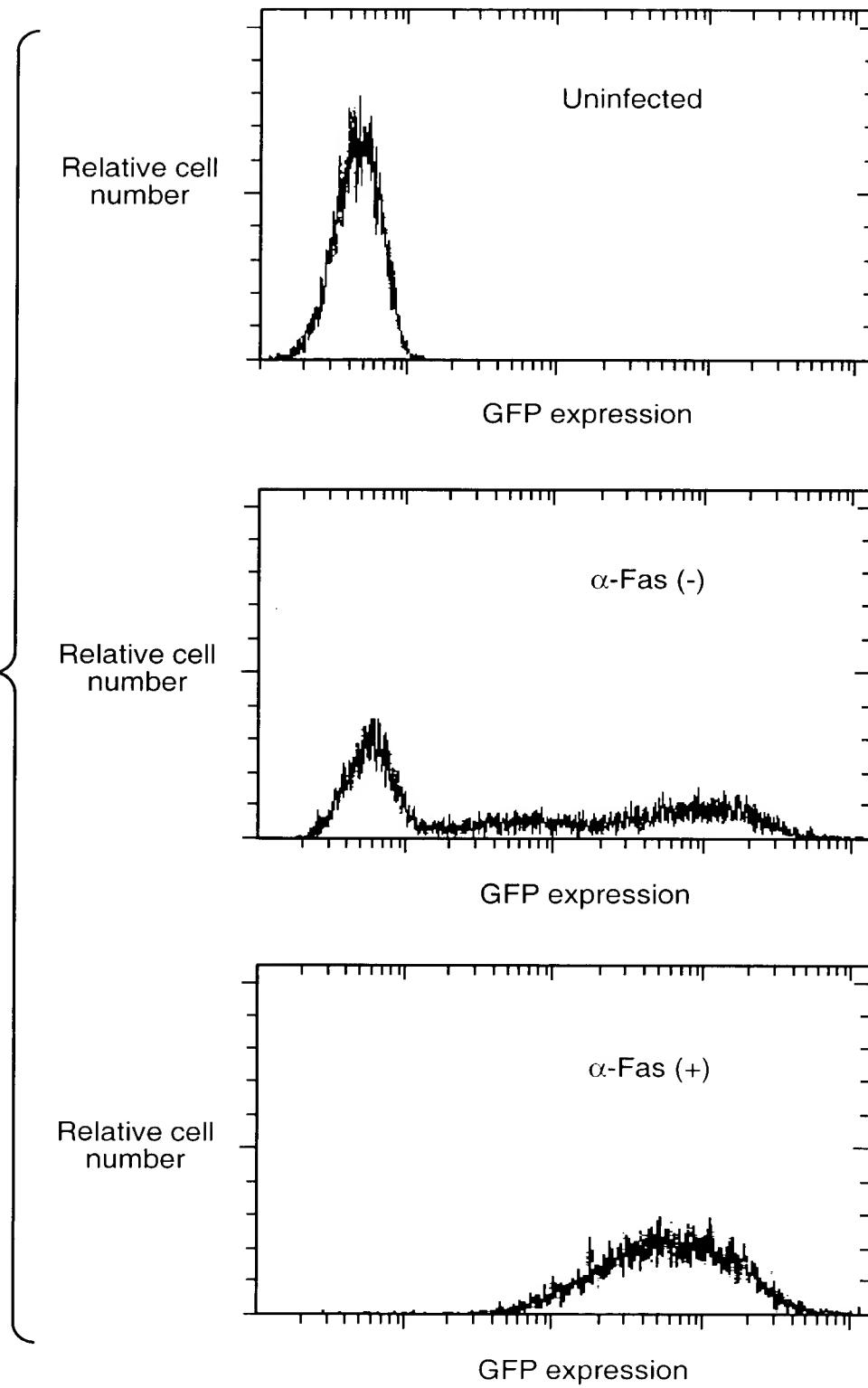
QPAAMMEDSDSDDYINVPA	-----
TEACTVVRDADNEPHTERPA	-----
QPAAPREEETGTEEYIMKMDL	-----

FIG.-3

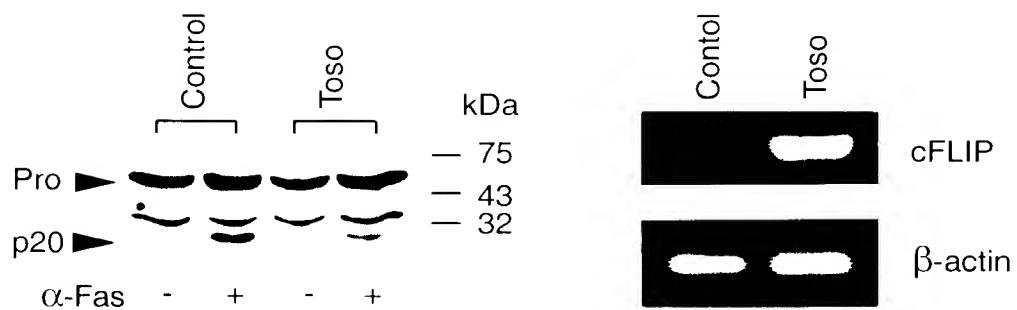
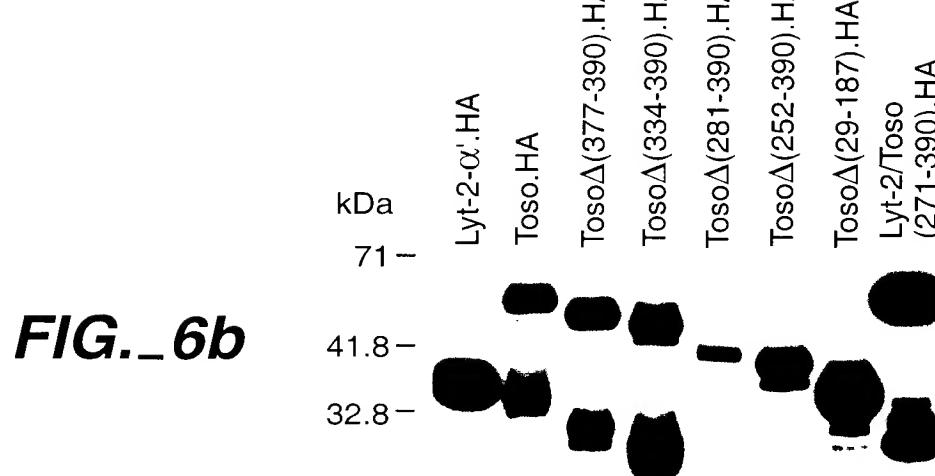
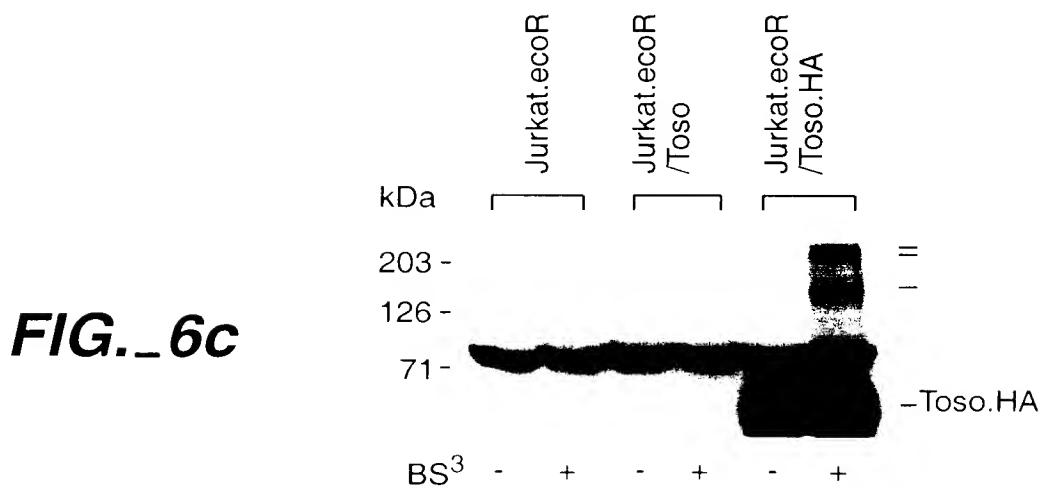
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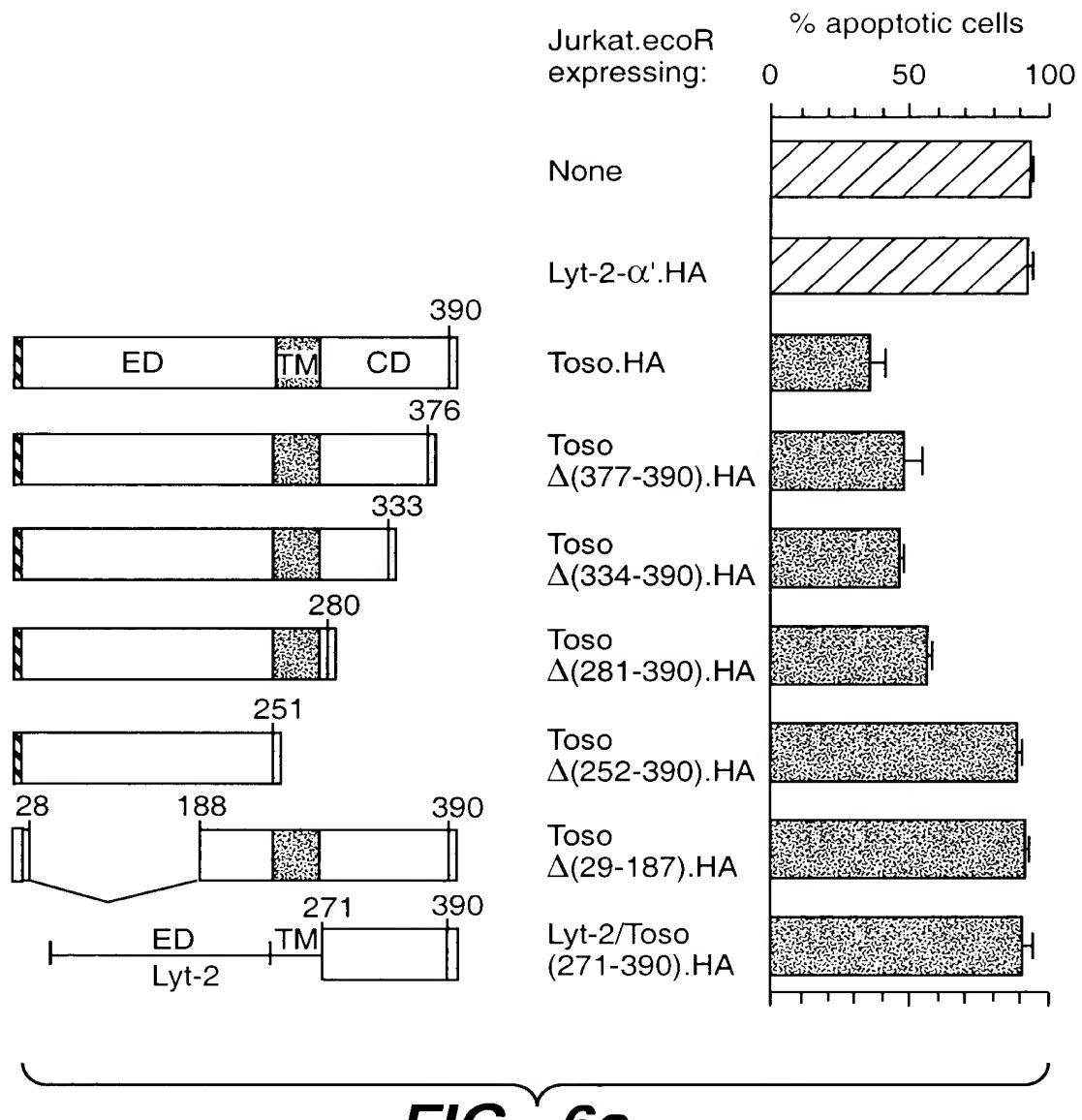
**FIG._4a****FIG._4b****FIG._4c****FIG._4d**

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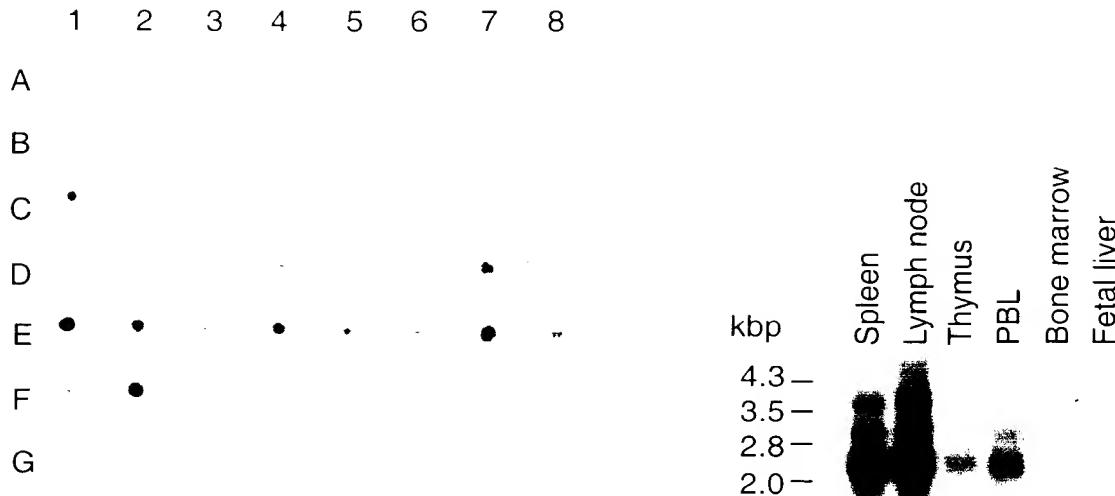
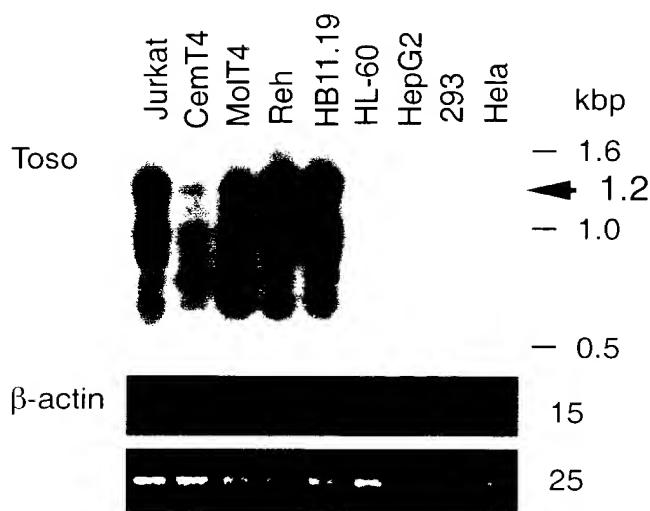
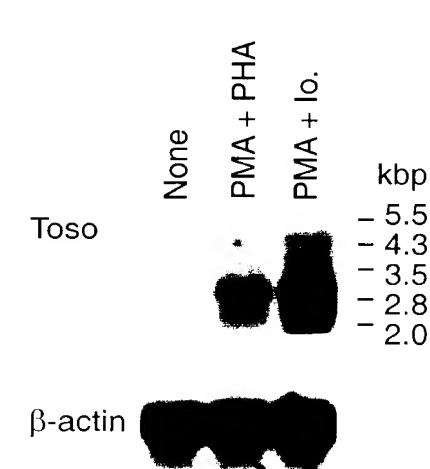
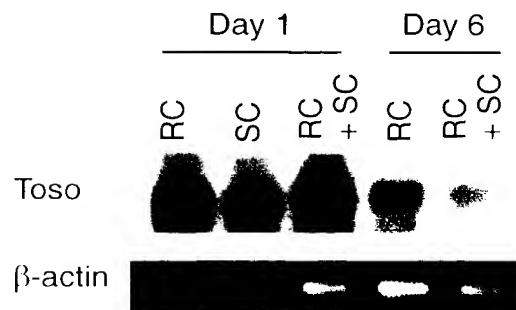
FIG._4e

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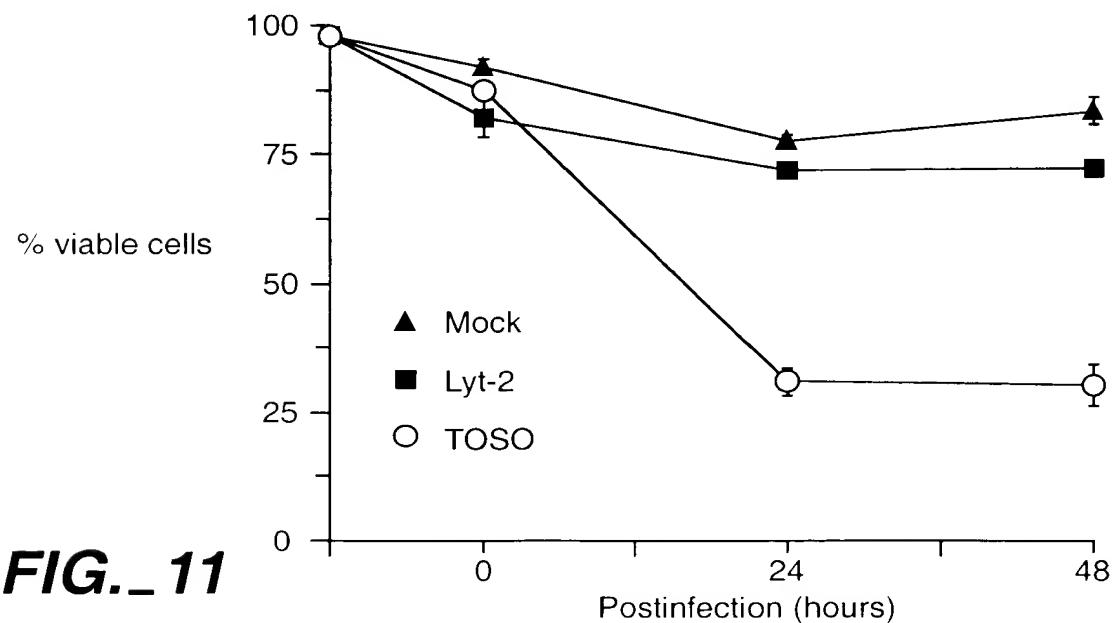
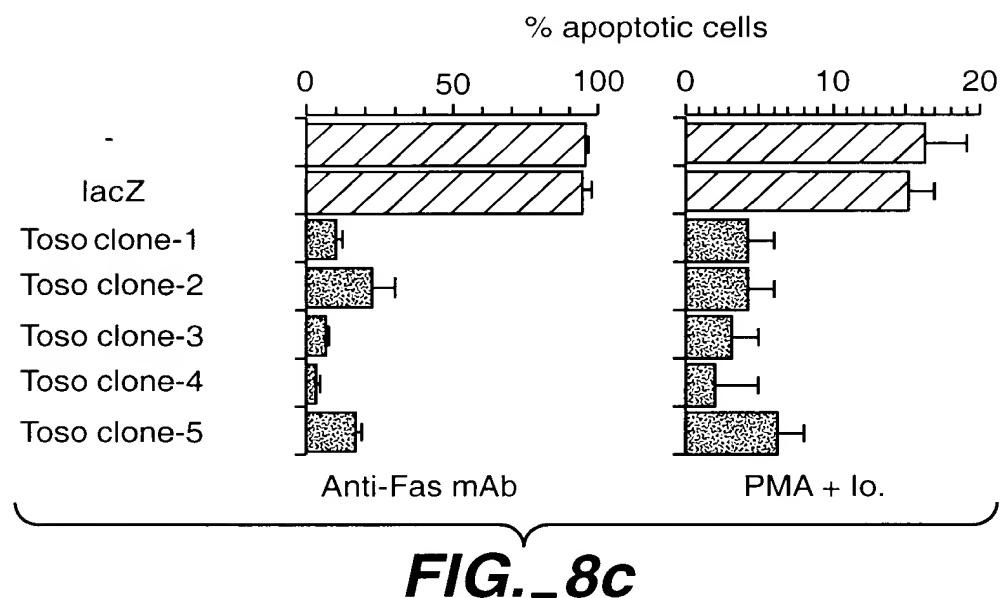
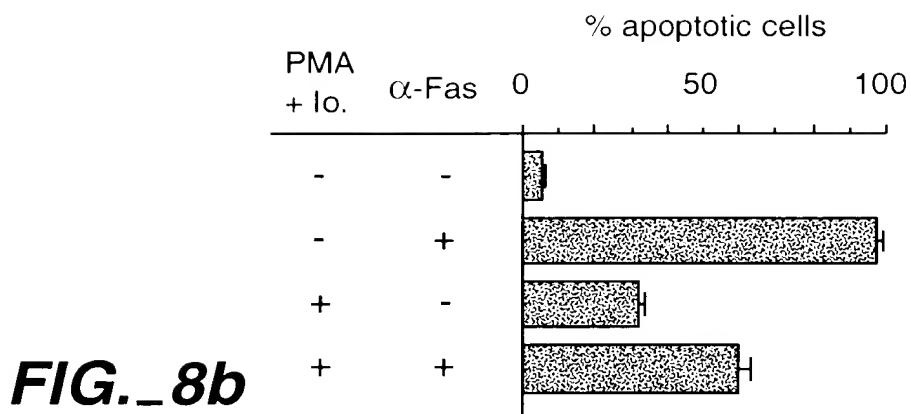
***FIG._5a******FIG._5b******FIG._6b******FIG._6c***



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**FIG._ 7a****FIG._ 7c****FIG._ 8a****FIG._ 9a****FIG._ 9b**

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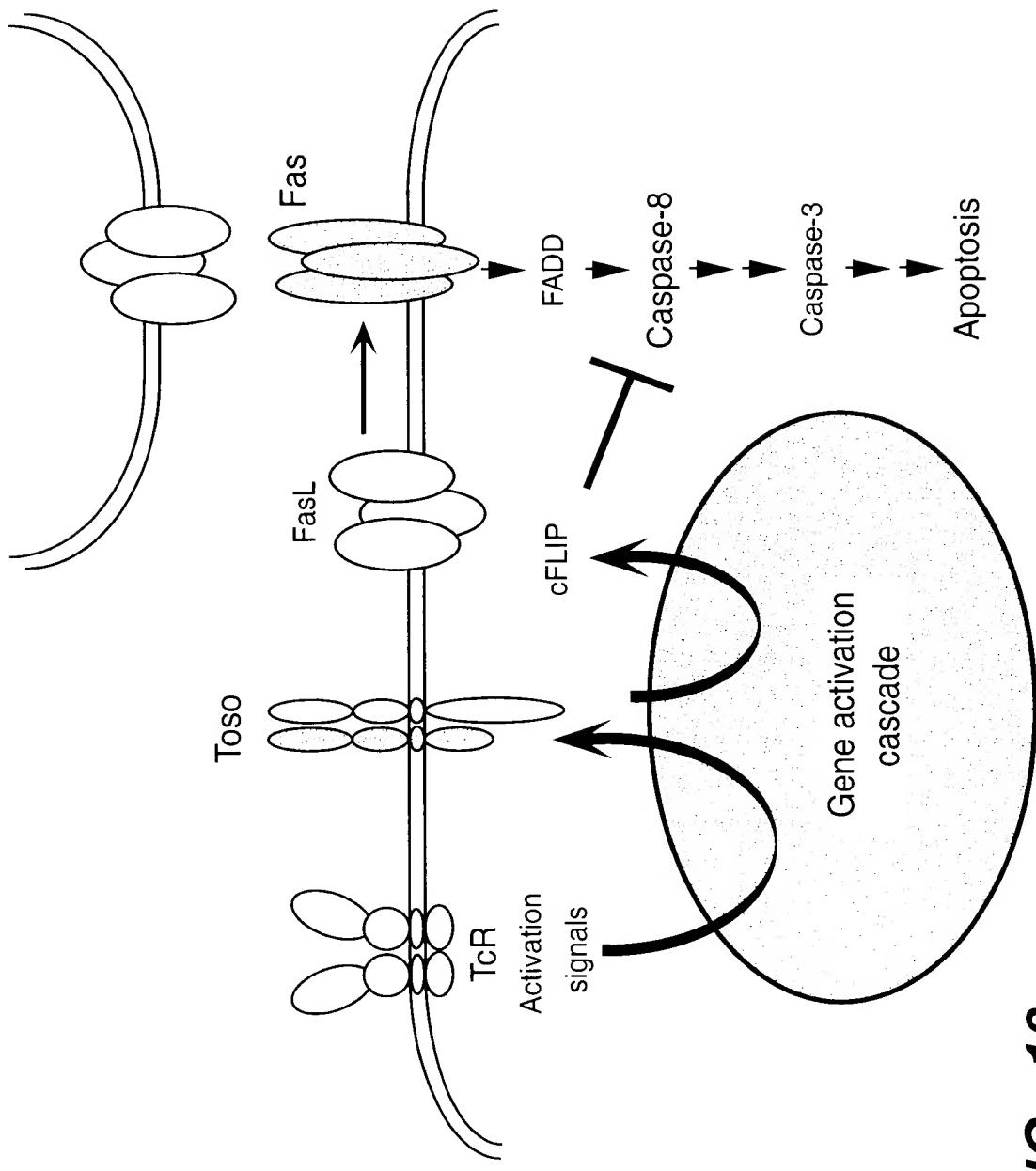


FIG._10